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SEQUENCE LISTING

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Maxygen, Inc.

<120> Methods and Compositions for Developing Spore Display
Systems for Medicinal and Industrial Applications

<130> 18097A-033520US

<140> US 10/028,247

<141> 2001-12-19

<150> US 60/214,161

<151> 2000-06-26

<150> US 09/892,208

<151> 2001-06-26

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 258

<212> DNA

<213> Bacillus subtilis

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<221> CDS

<222> (1)..(258)

<223> CotC27 including HA11 epitope region

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1 5 10 15

acg tat tat aag aag tat tac gaa tat gat aaa tct aga ggt acc tgc 96
Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
20 25 30

tat cct tat gat gtt cct gat tat gct tct tta gga tcc ctg cag aaa 144
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
35 40 45

gat tat gac tgt gat tac gac aaa aaa tat gat gac tat gat aaa aaa 192
Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
50 55 60

tat tat gat cac gat aaa aaa gac tat gat tat gtt gta gag tat aaa 240
Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
65 70 75 80

aag cat aaa aaa cac tac 258
Lys His Lys Lys His Tyr
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 <212> PRT
 <213> Bacillus subtilis

<220>
 <223> CotC27 including HA11 epitope region

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 Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
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 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
 35 40 45
 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
 50 55 60
 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
 65 70 75 80
 Lys His Lys Lys His Tyr
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 <213> Bacillus circulans

<220>
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 <222> (1)..(639)
 <223> lipase 396

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 1 5 10 15
 ctg tca gtc aca tcg ctg ttt gcg atg cag ccg tca gca aaa gcc gct 96
 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala
 20 25 30
 gaa cac aat cca gtt gtt atg gtt cac ggt atc gga gga gct tca tac 144
 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr
 35 40 45
 aat ttt gcg gga att aag agc tat ctc gta tct cag ggc tgg tca cgg 192
 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg
 50 55 60
 ggc aag ctg tat gcg gtt gat ttt tgg gac aag aca ggg acg aat tat 240
 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr
 65 70 75 80
 aac aat ggc ccg gta tta tca cga ttt gtg caa aag gtt tta gac gaa 288
 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu
 85 90 95
 acg ggt gcg aaa aaa gtg gat att gtc gct cac agc atg ggt ggc gcg 336
 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala
 100 105 110

aac aca ctt tac tac ata aaa aat ctg gac ggc gga aat aaa att gaa	384
Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
115 120 125	
aac gtc gta acg ctt ggc ggc gcg aac cgt ttg acg aca agc aag gcg	432
Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala	
130 135 140	
ctt ccg gga aca gat cca aat caa aag att tta tac aca tcc att tac	480
Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
145 150 155 160	
agc agt gcc gat atg att gtc atg aat tac tta tca aaa tta gac ggt	528
Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	
165 170 175	
gct aaa aac gtt caa att cat ggc gtt ggg cac att ggt tta ttg atg	576
Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met	
180 185 190	
aac agc caa gtc aac agc ctg att aaa gaa gga ctg aac ggc ggg ggc	624
Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly	
195 200 205	
ctc aat aca aat taa	639
Leu Asn Thr Asn	
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 <212> PRT
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<220>
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<400> 4

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Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr	
35 40 45	
Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg	
50 55 60	
Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr	
65 70 75 80	
Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu	
85 90 95	
Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala	
100 105 110	
Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
115 120 125	
Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Ser Lys Ala	
130 135 140	
Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
145 150 155 160	
Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	
165 170 175	

Ala	Lys	Asn	Val	Gln	Ile	His	Gly	Val	Gly	His	Ile	Gly	Leu	Leu	Met
			180					185					190		
Asn	Ser	Gln	Val	Asn	Ser	Leu	Ile	Lys	Glu	Gly	Leu	Asn	Gly	Gly	Gly
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Leu	Asn	Thr	Asn												
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 fusion protein

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<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 terminator

<400> 6
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